

SEQUENCE PROTOCOL

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5 <120> Nucleotide sequences which code for the metR and metZ genes

<130> 000369 BT

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<160> 8

<170> PatentIn Ver. 2.1

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<210> 1

<211> 2628

<212> DNA

<213> Corynebacterium glutamicum

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<220>

<221> CDS

<222> (447) .. (1013)

<223> metR gene

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<220>

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<222> (1038) .. (2183)

<223> metZ gene

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ggcagcaagc ccagcgccat taatcagagc ggtgaaataa acatgggttca tgattatgtc 180

aggacggtaa ttagacttat gaccagggtt aaggagggtca ccagggttgaa gccgcgctat 240

tgttccgtgg aaaagggggc cctgatctag ctgattattc atgcagtaa gcgctttcgg 300

taggtgggtg aatcatcgta gtcttccgag ccccgtagacc cgatccggtt tgtgcaatcc 360

aatgctactc ccacagagcg ggctactttc tctaaaaatg ttctcatagt agataaaatt 420

gttcttaaag cgacattatt gtctgc atg gaa gac gat ctc agt gct gct ctc 473

Met Glu Asp Asp Leu Ser Ala Ala Leu

1

5

gtc aaa gcg ctg ttc gac gcg cga acc caa cgc agg ctc tct atc tcg 521

Val Lys Ala Leu Phe Asp Ala Arg Thr Gln Arg Arg Leu Ser Ile Ser

10

15

20

25

gcg tta gct gaa tcc tcc ggt gtg tcg cga gca atg att tcc cgc gtg 569

Ala Leu Ala Glu Ser Ser Gly Val Ser Arg Ala Met Ile Ser Arg Val

30

35

40

SubA1

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	Glu Asn Ala Glu Ala Gln Pro Ser Ala Ala Leu Leu Gly Arg Leu Ser	
	45 50 55	
5	ggt gca ttg ggt atg acg ctt tcg gag ctc att gca cag gct gaa ggt	665
	Gly Ala Leu Gly Met Thr Leu Ser Glu Leu Ile Ala Gln Ala Glu Gly	
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10	ggc tat gac cgg ggc gct cgg cgg tca aag cag tct gta tgg aca gat	713
	Gly Tyr Asp Arg Gly Ala Arg Arg Ser Lys Gln Ser Val Trp Thr Asp	
	75 80 85	
15	cca gct acc ggt tac aca cgg cgt gca gtg tca cag ccg tca gaa tcc	761
	Pro Ala Thr Gly Tyr Thr Arg Arg Ala Val Ser Gln Pro Ser Glu Ser	
	90 95 100 105	
20	cca cta gaa cta gtg gaa gta atg ctg cct cct ggg gcg gaa gtt ggc	809
	Pro Leu Glu Leu Val Glu Val Met Leu Pro Pro Gly Ala Glu Val Gly	
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25	tac cca gct gat gct tat cgt ttc atg gat cag gtg gtc tgg gta ctc	857
	Tyr Pro Ala Asp Ala Tyr Arg Phe Met Asp Gln Val Val Trp Val Leu	
	125 130 135	
30	gaa ggg gcc gtt cgt att act gaa ggt gaa gag gtc cac gaa ctt tca	905
	Glu Gly Ala Val Arg Ile Thr Glu Gly Glu Glu Val His Glu Leu Ser	
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35	acg ggg gat tgt cta cgg ttt ggg cct ccg cga gat acc gac ttt gct	953
	Thr Gly Asp Cys Leu Arg Phe Gly Pro Pro Arg Asp Thr Asp Phe Ala	
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40	aat ccc acc acc gta gcc act agg tat tta gtt gcc ttg gac aag cgt	1001
	Asn Pro Thr Thr Val Ala Thr Arg Tyr Leu Val Ala Leu Asp Lys Arg	
	170 175 180 185	
45	gta cct cgt gct tgatataaca agtaaggaag cctg atg aat ttt tac cca	1052
	Val Pro Arg Ala Met Asn Phe Tyr Pro	
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50	cca tct gta cct att aac cct gcg tgg cgt cca ccc aca gta act gtg	1100
	Pro Ser Val Pro Ile Asn Pro Ala Trp Arg Pro Pro Thr Val Thr Val	
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55	caa gcg gga cgg cca gcc aga act cct ggt gcg ccg atg aac cca cct	1148
	Gln Ala Gly Arg Pro Ala Arg Thr Pro Gly Ala Pro Met Asn Pro Pro	
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60	atc acg ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg	1196
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65	cgc gat ggc aat gat gga tgg ggt gca ttt gag gct gcc atg gga act	1244
	Arg Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala Ala Met Gly Thr	
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70	cta gat ggt ggg ttc gcg gta tct tat tct tca ggt ttg gca gcg gca	1292
	Leu Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly Leu Ala Ala Ala	
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SubA1

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10	cgc	gga	agg	ctg	aag	gtt	cga	act	gtt	gat	gca	gac	aat	acc	gaa	gaa	1436
	Arg	Gly	Arg	Leu	Lys	Val	Arg	Thr	Val	Asp	Ala	Asp	Asn	Thr	Glu	Glu	
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15	gtg	att	gct	gct	gct	caa	ggt	gca	gat	gtg	gtg	tgg	gtg	gaa	tcg	atc	1484
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35	tcg	gca	acc	aaa	ctt	atc	ggt	gga	cat	tct	gat	ctt	ctt	ctt	gga	gtc	1676
	Ser	Ala	Thr	Lys	Leu	Ile	Gly	Gly	His	Ser	Asp	Leu	Leu	Leu	Gly	Val	
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40	gca	gtg	tgc	aag	tct	gag	cac	cat	gcg	cag	ttt	ctt	gcc	act	cac	cgt	1724
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45	cat	gat	cat	ggt	tca	gtg	ccg	gga	ggt	ctt	gaa	gcg	ttt	ctt	gct	ctc	1772
	His	Asp	His	Gly	Ser	Val	Pro	Gly	Gly	Leu	Glu	Ala	Phe	Leu	Ala	Leu	
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50	cgt	gga	ttg	tat	tcc	ttg	gcg	gtg	cgt	ctt	gat	cga	gca	gaa	tcc	aac	1820
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	Ala	Ala	Glu	Leu	Ser	Arg	Arg	Leu	Asn	Ala	His	Pro	Ser	Val	Thr	Arg	
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60	gtc	aat	tat	cca	gga	ctt	cct	gat	gat	ccc	caa	cat	gaa	aaa	gcc	gtg	1916
	Val	Asn	Tyr	Pro	Gly	Leu	Pro	Asp	Asp	Pro	Gln	His	Glu	Lys	Ala	Val	
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65	cga	gtc	cta	ccc	tct	gga	tgt	gga	aac	atg	ttg	tca	ttt	gag	ctt	gat	1964
	Arg	Val	Leu	Pro	Ser	Gly	Cys	Gly	Asn	Met	Leu	Ser	Phe	Glu	Leu	Asp	
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SubA1

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10 acc cac gcg acc agt tgg gga ggt gtg gaa aca gcc att gaa cgt cgc 2060
 Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala Ile Glu Arg Arg
 515 520 525 530

15 acc agg cgg gat gct gaa gtg gtg gca gga gta ccg atg act ctt tgc 2108
 Thr Arg Arg Asp Ala Glu Val Val Ala Gly Val Pro Met Thr Leu Cys
 535 540 545

20 cgc gtt tcc gta gga att gaa gac gtt gaa gat cta tgg gaa gac ctc 2156
 Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu Trp Glu Asp Leu
 550 555 560

25 aac gcc tca atc gac aaa gtt ctg ggt tagaactcgt agccagtaac 2203
 Asn Ala Ser Ile Asp Lys Val Leu Gly
 565 570

30 cagaccttca gtgtttgggt gccactcag tgctggggcg acatgatcag cgaagttctt 2263
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 <213> Corynebacterium glutamicum

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 35 40 45
 50 Ser Ala Ala Leu Leu Gly Arg Leu Ser Gly Ala Leu Gly Met Thr Leu
 50 55 60
 Ser Glu Leu Ile Ala Gln Ala Glu Gly Gly Tyr Asp Arg Gly Ala Arg
 65 70 75 80
 Arg Ser Lys Gln Ser Val Trp Thr Asp Pro Ala Thr Gly Tyr Thr Arg
 85 90 95
 55 Arg Ala Val Ser Gln Pro Ser Glu Ser Pro Leu Glu Leu Val Glu Val
 100 105 110
 Met Leu Pro Pro Gly Ala Glu Val Gly Tyr Pro Ala Asp Ala Tyr Arg
 115 120 125
 60 Phe Met Asp Gln Val Val Trp Val Leu Glu Gly Ala Val Arg Ile Thr
 130 135 140

Glu	Gly	Glu	Glu	Val	His	Glu	Leu	Ser	Thr	Gly	Asp	Cys	Leu	Arg	Phe
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Gly	Pro	Pro	Arg	Asp	Thr	Asp	Phe	Ala	Asn	Pro	Thr	Thr	Val	Ala	Thr
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65					70				75						80
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Ala	Ile	Val	Asp	Gly	Val	Arg	Gly	Leu	Gly	Val	Leu	Thr	Val	Val	Asp
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Ala	Thr	Phe	Ala	Thr	Pro	Leu	Arg	Gln	Arg	Pro	Leu	Glu	Leu	Gly	Ala
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SubA1

Ala Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Gly Val
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<223> Description of the artificial sequence: Primer orfR 20

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gtaattagac ttatgaccag gtttaaggag gtcaccaggt tgaagccgcg ctattgttcc 180
gtggaaaagg gggccctgat ctatgtgatt attcatcgca gtaagcgctt tccgtaggtg 240
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 <212> DNA
 <213> Artificial sequence

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